

OIKE

RAW SEQUENCE LISTING

DATE: 06/20/2001

PATENT APPLICATION: US/09/697,206A

TIME: 14:36:16

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\06202001\I697206A.raw

ENTERED

4 <110> APPLICANT: Daniel E.H. Afar
5 Arthur B. Raitano
6 Rene S. Hubert
7 Steve Chappell Mitchell
8 Aya Jakobovits
10 <120> TITLE OF INVENTION: NOVEL GENE UPREGULATED IN CANCERS OF THE
11 PROSTATE
13 <130> FILE REFERENCE: 129.21-US-U1
15 <140> CURRENT APPLICATION NUMBER: 09/697,206A
C--> 16 <141> CURRENT FILING DATE: 2001-06-04
18 <150> PRIOR APPLICATION NUMBER: 60/162,364
19 <151> PRIOR FILING DATE: 1999-10-28
21 <160> NUMBER OF SEQ ID NOS: 26
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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26 <211> LENGTH: 3585
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo Sapiens
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33 gtgctagtta gaccgatca gttggaactg acggaggact gcaaagaaga aactaaaata 180
34 gacgtcgaaa gcctgtcctc ggcgctcgag ctggaccaag ccctccgaca gtttaaccag 240
35 tcagttagca atgaactgaa tattggagta gggacttccct tctgtctctg tactgatggg 300
36 cagcttcatg tcaggcaaat cctgcctcct gaggcttcca agaagaatgt actattacct 360
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38 cctgatattg acaaactgga cgttgccaca atgacagagt atttaaattt tgagaagagt 480
39 agttcagtct ctcgatatgg agcctctcaa gttgaagata tggggaatat aatttttagca 540
40 atgatttcag agccttataa tcacagggtt tcagatccag agagagtga ttacaagttt 600
41 gaaagtggaa cttgcagcaa gatggaactt attgatgata acaccgtagt cagggcacga 660
42 ggtttaccat ggcagtcttc agatcaagat attgcaagat tcttcaaagg actcaatatt 720
43 gccaaaggag gtgcagcact ttgtctgaat gctcagggtc gaaggaacgg agaagctctg 780
44 gttaggtttg taagtgagga gcaccgagac ctagcactac agaggcaca acatcacatg 840
45 gggaccgggt atattgaggt ttacaaagca acagggtgaag atttccttaa aattgctggg 900
46 ggtacttcca atgaggtagc ccagtttctc tccaaggaaa atcaagtcac tgttcgcatg 960
47 cgggggctcc ctttccacggc cacagctgaa gaagtgggtg ccttcttttg acagcattgc 1020
48 cctattactg ggggaaagga aggcctcctc tttgtcacct acccagatgg taggccaaca 1080
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50 aaagacttgt tgggtaaaag atacattgaa ctcttcagga gcacagcagc tgaagttcag 1200
51 caggtgctga atcgattctc ctcgccccct ctcatccac ttccaacccc tcccattatt 1260
52 ccagtactac ctacgcaatt tgtgccccct acaaatgtta gagactgtat acgccttcca 1320
53 ggtcttccct atgcagccac aattgaggac atcctggatt tcctggggga gttcgccaca 1380
54 gatattcgta ctcatggggt tcacatgggt ttgaatcacc agggccgccc atcaggagat 1440
55 gcctttatcc agatgaagtc tgcggacaga gcatttatgg ctgcacagaa gtgtcataaa 1500
56 aaaaacatga aggacagata tgttgaagtc tttcagtgtt cagctgagga gatgaacttt 1560
57 gtgttaaatg ggggcacttt aaatcgaaat ggcttatccc caccgccatg cctgtctcct 1620
58 cctctctaca catttcacgc tctgtctgca gttattccta cagaagctgc catttaccag 1680

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59 ccctctgtga ttttgaatcc acgagcactg cagccctoca cagcgtacta cccagcaggc 1740
60 actcagctct tcatgaacta cacagcgtac tatcccagcc cccaggttc gcctaatagt 1800
61 cttggctact tccctacagc tgctaattctt agcgggtgtcc ctccacagcc tggcacggtg 1860
62 gtcagaatgc agggcctggc ctacaatact ggagttaagg aaattcttaa cttcttccaa 1920
63 ggttaccagt atgcaaccga ggatggactt atacacacaa atgaccaggc caggactcta 1980
64 cccaaagaat gggtttgtat ttaagggccc cagcagttag aacatcctca gaaaagaagt 2040
65 gtttgaaaga tgtatggtga tcttgaaacc tccagacaca agaaaacttc tagcaaattc 2100
66 aggggaagtt tgtctacact caggctgcag tattttcagc aaacttgatt ggacaaacgg 2160
67 gcctgtgcct tatcttttgg tggagtgaag aaatttgagc tagtgaagcc aaatcgtaac 2220
68 ttacagcaag cagcatgcag catacctggc tctttgctga ttgcaaatag gcatttaaaa 2280
69 tgtgaatttg gaatcagatg tctccattac ttccagttaa agtggcatca taggtgtttc 2340
70 ctaagtttta agtcttggat aaaaactcca ccagtgtota ccatctccac catgaactct 2400
71 gttaaggaag cttcattttt gtatatcccc gctcttttct cttcatttcc ctgtcttctg 2460
72 cataatcatg ccttcttgct aagtaattca agcataagat cttggaataa taaaatcaca 2520
73 atcttaggag aaagaataaa attgttattt tcccagtcct ttggccatga tgatatctta 2580
74 tgattaaaaa caaattaaat tttaaaacac ctgaagataa attagaagaa attgtgcacc 2640
75 ctccacaaaa catacaaagt ttaaaagttt ggatcttttt ctacgcaggt atcagttgta 2700
76 aataatgaat tagggggccaa aatgcaaaac gaaaaatgaa gcagctacat gtagttagta 2760
77 atttctagtt tgaactgtaa ttgaatattg tggcttcata tgtattattt tatattgtac 2820
78 ttttttcatt attgatggtt tggactttta taagagaaat tccatagttt ttaatatccc 2880
79 agaagtgaga caatttgaac agtgtattct agaaaaaat acactaactg aacagaagtg 2940
80 aatgcttata tatattatga tagccttaaa ccttttttct ctaatgcctt aactgtcaaa 3000
81 taattataac cttttaaagc ataggactat agtcagcatg ctagactgag aggtaaacac 3060
82 tgatgcaatt agaacaggta ctgatgctgt cagtgtttta cactatgttt agctgtgttt 3120
83 atgctataaa agtgcaatat tagacactag ctagtactgc tgcctcatgt aactccaaag 3180
84 aaaacaggat ttcattaagt gcattgaatg tggatatatt tctaagttac tcatattgtc 3240
85 ctttgcttga atgcaatgcc gtgcagattt atgaggctgc tattttttatt ttctgtgcat 3300
86 tactttaaca ccttaaaggg agaagcaaac atttccctct tcagctgact ggcaatggcc 3360
87 ctttaactgc aataggaaga aaaaaaaaaa ggtttgtgtg aaaattggtg ataactggca 3420
88 cttaaagatcg aaaagaaatt tctgtatact tgatgcctta agatgcccaa agctgcccaa 3480
89 agctctgaaa gactttaaga taggcagtaa tgcttactac aatactactg agtttttcta 3540
90 gagttaacat ttgataataa aacttgccctg ttaaatctca aaaaa 3585

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92 <210> SEQ ID NO: 2

93 <211> LENGTH: 517

94 <212> TYPE: PRT

95 <213> ORGANISM: Homo Sapiens

97 <400> SEQUENCE: 2

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98 Met Thr Glu Tyr Leu Asn Phe Glu Lys Ser Ser Ser Val Ser Arg Tyr
99 1 5 10 15
100 Gly Ala Ser Gln Val Glu Asp Met Gly Asn Ile Ile Leu Ala Met Ile
101 20 25 30
102 Ser Glu Pro Tyr Asn His Arg Phe Ser Asp Pro Glu Arg Val Asn Tyr
103 35 40 45
104 Lys Phe Glu Ser Gly Thr Cys Ser Lys Met Glu Leu Ile Asp Asp Asn
105 50 55 60
106 Thr Val Val Arg Ala Arg Gly Leu Pro Trp Gln Ser Ser Asp Gln Asp
107 65 70 75 80
108 Ile Ala Arg Phe Phe Lys Gly Leu Asn Ile Ala Lys Gly Gly Ala Ala
109 85 90 95

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110 Leu Cys Leu Asn Ala Gln Gly Arg Arg Asn Gly Glu Ala Leu Val Arg
111          100          105          110
112 Phe Val Ser Glu Glu His Arg Asp Leu Ala Leu Gln Arg His Lys His
113          115          120          125
114 His Met Gly Thr Arg Tyr Ile Glu Val Tyr Lys Ala Thr Gly Glu Asp
115          130          135          140
116 Phe Leu Lys Ile Ala Gly Gly Thr Ser Asn Glu Val Ala Gln Phe Leu
117 145          150          155          160
118 Ser Lys Glu Asn Gln Val Ile Val Arg Met Arg Gly Leu Pro Phe Thr
119          165          170          175
120 Ala Thr Ala Glu Glu Val Val Ala Phe Phe Gly Gln His Cys Pro Ile
121          180          185          190
122 Thr Gly Gly Lys Glu Gly Ile Leu Phe Val Thr Tyr Pro Asp Gly Arg
123          195          200          205
124 Pro Thr Gly Asp Ala Phe Val Leu Phe Ala Cys Glu Tyr Ala Gln
125          210          215          220
126 Asn Ala Leu Arg Lys His Lys Asp Leu Leu Gly Lys Arg Tyr Ile Glu
127 225          230          235          240
128 Leu Phe Arg Ser Thr Ala Ala Glu Val Gln Gln Val Leu Asn Arg Phe
129          245          250          255
130 Ser Ser Ala Pro Leu Ile Pro Leu Pro Thr Pro Pro Ile Ile Pro Val
131          260          265          270
132 Leu Pro Gln Gln Phe Val Pro Pro Thr Asn Val Arg Asp Cys Ile Arg
133          275          280          285
134 Leu Arg Gly Leu Pro Tyr Ala Ala Thr Ile Glu Asp Ile Leu Asp Phe
135          290          295          300
136 Leu Gly Glu Phe Ala Thr Asp Ile Arg Thr His Gly Val His Met Val
137 305          310          315          320
138 Leu Asn His Gln Gly Arg Pro Ser Gly Asp Ala Phe Ile Gln Met Lys
139          325          330          335
140 Ser Ala Asp Arg Ala Phe Met Ala Ala Gln Lys Cys His Lys Lys Asn
141          340          345          350
142 Met Lys Asp Arg Tyr Val Glu Val Phe Gln Cys Ser Ala Glu Glu Met
143          355          360          365
144 Asn Phe Val Leu Met Gly Gly Thr Leu Asn Arg Asn Gly Leu Ser Pro
145          370          375          380
146 Pro Pro Cys Leu Ser Pro Pro Ser Tyr Thr Phe Pro Ala Pro Ala Ala
147 385          390          395          400
148 Val Ile Pro Thr Glu Ala Ala Ile Tyr Gln Pro Ser Val Ile Leu Asn
149          405          410          415
150 Pro Arg Ala Leu Gln Pro Ser Thr Ala Tyr Tyr Pro Ala Gly Thr Gln
151          420          425          430
152 Leu Phe Met Asn Tyr Thr Ala Tyr Tyr Pro Ser Pro Pro Gly Ser Pro
153          435          440          445
154 Asn Ser Leu Gly Tyr Phe Pro Thr Ala Ala Asn Leu Ser Gly Val Pro
155          450          455          460
156 Pro Gln Pro Gly Thr Val Val Arg Met Gln Gly Leu Ala Tyr Asn Thr
157 465          470          475          480
158 Gly Val Lys Glu Ile Leu Asn Phe Phe Gln Gly Tyr Gln Tyr Ala Thr

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159           485           490           495
160 Glu Asp Gly Leu Ile His Thr Asn Asp Gln Ala Arg Thr Leu Pro Lys
161           500           505           510
162 Glu Trp Val Cys Ile
163           515
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166 <211> LENGTH: 14
167 <212> TYPE: DNA
168 <213> ORGANISM: Artificial Sequence
170 <220> FEATURE:
171 <223> OTHER INFORMATION: Primer
173 <400> SEQUENCE: 3
174 ttttgatcaa gctt                                     14
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177 <211> LENGTH: 42
178 <212> TYPE: DNA
179 <213> ORGANISM: Artificial Sequence
181 <220> FEATURE:
182 <223> OTHER INFORMATION: Adaptor
184 <400> SEQUENCE: 4
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187 <210> SEQ ID NO: 5
188 <211> LENGTH: 12
189 <212> TYPE: DNA
190 <213> ORGANISM: Artificial Sequence
192 <220> FEATURE:
193 <223> OTHER INFORMATION: Adaptor
195 <400> SEQUENCE: 5
196 ggcccgtcct ag                                       12
198 <210> SEQ ID NO: 6
199 <211> LENGTH: 40
200 <212> TYPE: DNA
201 <213> ORGANISM: Artificial Sequence
203 <220> FEATURE:
204 <223> OTHER INFORMATION: Adaptor
206 <400> SEQUENCE: 6
207 gtaatacgac tcactatagg gcagcgtggt cgcggccgag      40
209 <210> SEQ ID NO: 7
210 <211> LENGTH: 10
211 <212> TYPE: DNA
212 <213> ORGANISM: Artificial Sequence
214 <220> FEATURE:
215 <223> OTHER INFORMATION: Adaptor
217 <400> SEQUENCE: 7
218 cggctcctag                                       10
220 <210> SEQ ID NO: 8
221 <211> LENGTH: 22
222 <212> TYPE: DNA
223 <213> ORGANISM: Artificial Sequence

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225 <220> FEATURE:
226 <223> OTHER INFORMATION: Primer
228 <400> SEQUENCE: 8
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231 <210> SEQ ID NO: 9
232 <211> LENGTH: 22
233 <212> TYPE: DNA
234 <213> ORGANISM: Artificial Sequence
236 <220> FEATURE:
237 <223> OTHER INFORMATION: Primer
239 <400> SEQUENCE: 9
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242 <210> SEQ ID NO: 10
243 <211> LENGTH: 20
244 <212> TYPE: DNA
245 <213> ORGANISM: Artificial Sequence
247 <220> FEATURE:
248 <223> OTHER INFORMATION: Primer
250 <400> SEQUENCE: 10
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254 <211> LENGTH: 25
255 <212> TYPE: DNA
256 <213> ORGANISM: Homo Sapiens
258 <400> SEQUENCE: 11
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261 <210> SEQ ID NO: 12
262 <211> LENGTH: 26
263 <212> TYPE: DNA
264 <213> ORGANISM: Homo Sapiens
266 <400> SEQUENCE: 12
267 agccacacgc agtcattgt agaagg 26
269 <210> SEQ ID NO: 13
270 <211> LENGTH: 24
271 <212> TYPE: DNA
272 <213> ORGANISM: Artificial Sequence
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275 <223> OTHER INFORMATION: Primer
277 <400> SEQUENCE: 13
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281 <211> LENGTH: 24
282 <212> TYPE: DNA
283 <213> ORGANISM: Artificial Sequence
285 <220> FEATURE:
286 <223> OTHER INFORMATION: Primer
288 <400> SEQUENCE: 14
289 ggagatggta gacactggtg gagt 24
291 <210> SEQ ID NO: 15

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VERIFICATION SUMMARY

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L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date